SEOUENCE LISTING

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<110> CuraGen Corporation et al.
      Alsobrook II, John P.
      Eichen, Joseph
      Lepley, Denise M.
      Miller, Charles E.
      Mezes, Peter
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Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn

130 135 140

Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly 150 155 Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly 170 Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr <210> 14 <211> 612 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(609) <400> 14 ggt ttc ctg ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac 48 Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His 10 tte ctq ctq ccq ccq qct qgt gaa cgt ccg cca ctg ctg ggt gaa cgt 96 Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg 144 Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Pro Gly Ala Ala Gln 40 45 35 ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt 192 Leu Ala His Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys Arg 50 55 act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc 240 Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr 65 70 cqt caq qac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct 288 Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly 100 105 atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa 384 Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu 115 tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct 432

Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser

130 135 140

480

576

612

tee aac ate tae aaa cat ggt gae ace gge egt ege tae tte gtt get Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala 145 ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His 170 165 cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val 180 185 cca gaa ctg tat aaa aac ctg ctg atg tac acc taa Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 195 <210> 15 <211> 203 <212> PRT <213> Homo sapiens <400> 15 Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg 25 Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala 90 Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly 100 105 Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu 120 Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser 130 135 Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr

195 200

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	ccg Pro														96
	gaa Glu														144
_	cat His 50			_	-	_	_	_	_	_	_				192
	ctg Leu														240
	tct Ser										-	-		-	288
-	tct Ser		_		_	-			_			_		-	336
	ggc Gly														384
	gaa Glu 130														432
	aaa Lys														480
	ggt Gly														528
	cac His		_	_	_		_	_	_	 _	_		_	_	576
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Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp
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Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile
                        135
Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys
Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe
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Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu
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Tyr Lys Asn Leu Leu Met Tyr Thr
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Tyr Lys Asn Leu Leu Met Tyr Thr

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			t cag ctg gct a Gln Leu Ala		
	-		c cgt act ggt s Arg Thr Gly 60		-
		· Val Gln Gl	t acc cgt cag y Thr Arg Gln 75	-	-
			t gct gtt ggt 1 Ala Val Gly 90		
Arg Gly Val A			g ggt atg aac u Gly Met Asn 5		
			et gaa tgc atc er Glu Cys Ile		
			c tct tcc aac r Ser Ser Asn 140		
		g Tyr Phe Va	t gct ctg aac 1 Ala Leu Asn 155		
		_	t cac cag aaa g His Gln Lys 170		
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ctg ctg atg t Leu Leu Met T 195		i			594
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Ser	Ala		Gly	Gly	Pro	Gly		Ala	Gln	Leu	Ala		Leu	His	Gly	
	_	35	_	_		_	40	_	_	eter T	~3	45			a 1	
Ile	Leu 50	Arg	Arg	Arg	Gin	Leu 55	Tyr	Cys	Arg	Thr	60 GIÀ	Pne	His	Leu	Gin	
Ile 65	Leu	Pro	Asp	Gly	Ser 70	Val	Gln	Gly	Thr	Arg 75	Gln	Asp	His	Ser	Leu 80	
Phe	Gly	Ile	Leu	Glu 85	Phe	Ile	Ser	Val	Ala 90	Val	Gly	Leu	Val	Ser 95	Ile	
Arg	Gly	Val	Asp 100	Ser	Gly	Leu	Tyr	Leu 105	Gly	Met	Asn	Asp	Lys 110	Gly	Glu	
Leu	Tyr	Gly 115	Ser	Glu	Lys	Leu	Thr 120	Ser	Glu	Cys	Ile	Phe 125	Arg	Glu	Gln	
Phe	Glu 130	Glu	Asn	Trp	Tyr	Asn 135	Thr	Tyr	Ser	Ser	Asn 140	Ile	Tyr	Lys	His	
Gly 145	Asp	Thr	Gly	Arg	Arg 150	Tyr	Phe	Val	Ala	Leu 155	Asn	Lys	Asp	Gly	Thr 160	
Pro	Arg	Asp	Gly	Ala 165	Arg	Ser	Lys	Arg	His 170	Gln	Lys	Phe	Thr	His 175	Phe	
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	cgc Arg															96
	ctg Leu															144
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gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac 384 Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr 115 120 125

tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt 432 Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val 130 135 140

gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt 480 Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg 145 150 155 160

cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt $$ 528 His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg $$ 165 $$ 170 $$ 175

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Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys 35 40 45

Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly 50 55 60

Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val
65 70 75 80

Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu 85 90 95

Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser
100 105 110

Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr 115 120 125

Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val

130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg 145 150 150 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg
165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 180 185

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<212> DNA

<213> Homo sapiens

<400> 22

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<212> PRT

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Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
50 55 . 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln 65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe 115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn 130 135 140

Leu Leu Met Tyr Thr

145

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cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360
tctaacatat ataaacatgg agacactggc cgcaggtatt ttgtggcact taacaaagac 420
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